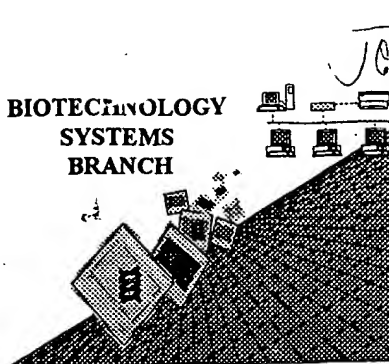


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/762,267  
Source: PCR/09  
Date Processed by STIC: 7/11/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

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### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,767

DATE: 07/11/2001

TIME: 11:19:54

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07112001\I762767.raw

Does Not Comply  
Corrected Diskette Needed

## SEQUENCE LISTING

2 (1) GENERAL INFORMATION:

C--> 3 (i) APPLICANT:

4 SCHMIDT, Harald

5 ZABEL, Ulrike

6 POLLER, Wolfgang

W--> 8 (ii) TITLE OF INVENTION: Isolated and purified human soluble

9 guanylyl cyclase  $\alpha 1/\alpha 1$  (hsGC $\alpha 1/\alpha 1$ )

E--> 10 (iii) VOS-101

11 (iv) US 09/762,767

W--> 12 2001-02-13

W--> 13 (iv) PCT/DE99/02601

W--> 14 1999-08-16

W--> 15 (iv) DE 198 37 015.6

W--> 16 1998-08-14

E--> 22 (iii) NUMBER OF SEQUENCES: 10

C--> 24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

C--> 0 (vi) CURRENT APPLICATION DATA:

C--> 0 (A) APPLICATION NUMBER: US/09/762,767

C--> 0 (B) FILING DATE: 13-Feb-2001

Completelyinvalidformat fora U.S.case.(see attached)

## ERRORED SEQUENCES

E--> 30 (2) DATA TO SEQ ID NO: 1:

E--> 0 (2) INFORMATION FOR SEQ ID NO:

31 (i) SEQUENCE CHARACTERISTICS:

32 (A) LENGTH: 3015 basepairs

33 (B) TYPE: nucleotide

34 (C) STRANDEDNESS: doublestrand

35 (D) TOPOLOGY: linear

37 (ii) MOLECULE TYPE: genomic DNA

0 (D) DEVELOPMENTAL STAGE: 1:

E--> 39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

EPO format is  
invalid for U.S.  
case

41	CCCTTATGGC	GATTGGGCGG	CTGCAGAGAC	CAGGACTCAG	TTCCCCTGCC	CTAGTCTGAG	60
42	CCTAGTGGGT	GGGACTCAGC	TCAGAGTCAG	TTTTCCAGAA	GCAGGTTTCA	GTGCAGAGTT	120
43	TTCCTACACT	TTTCTGCGC	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	GGCGGAGGAC	180
44	ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGGCG	TGATCTCACC	240
45	ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	CAGCCCCGAG	300
46	GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	GCCACCGCGG	360
47	TCTCCGCGCC	TGCTGTCACC	CTGTCGCCCTG	AGCTGCCTGA	CAGTGACAAAT	GACATCCCAG	420
48	TTACCAAGTG	CCTTGAATTG	ATAGTGGCTT	CTGTTTGTCA	GTCTCATATA	AGAACTACAG	480
49	CTCATCAGGA	GGAGATCGCA	GCAGGGTAAG	AGACACCAAC	ACCATGTTCT	GCACGAAGCT	540

09/762,767 1

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

### (i) APPLICANTS:

SCHMIDT, Harald  
ZABEL, Ulrike  
POLLER, Wolfgang

*move up - all responses must be on same line as heading*

(ii) TITLE OF THE INVENTION: Isolated and purified human soluble guanylyl cyclase  $\alpha 1/\beta 1$  (hsGC $\alpha 1/\beta 1$ )

(iii) ~~VOS-101~~

*delete*  
*delete all accent marks - they cannot be processed in the CRF program*  
*NUMBER OF SEQUENCES: 10 - insert this and go under CURRENT APPLICATION DATA*

(vi) ~~US 09/762,767~~  
2001-02-13

(vii) ~~PCT/DE99/02601~~  
1999-08-16

(viii) ~~DE 198 37 015.6~~  
1998-08-14

*Move these (go under PRIOR APPLICATION DATA)*

(iii) ~~10~~ NUMBER OF SEQUENCES: 10

### (j) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(v) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE:  
(B) STREET:  
(C) CITY:  
(D) STATE:  
(E) COUNTRY:  
(F) ZIP:

*insert these mandatory headers and responses for all U.S. cases*

### (2) INFORMATION FOR SEQ ID NO: 1:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3015 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double strand
- (D) TOPOLOGY: linear

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCTTATGGC	GATTGGGCGG	CTGCAGAGAC	CAGGACTCAG	TTCCCCTGCC	CTAGTCTGAG	60
CCTAGTGGGT	GGGACTCAGC	TCAGAGTCAG	TTTTCCAGAA	GCAGGTTTCA	GTGCAGAGTT	120
TTCCTACACT	TTTCCTGCGC	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	GGCGGAGGAC	180
ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGGCG	TGATCTCACC	240
ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	CAGCCCCGAG	300
GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	GCCACCGCGG	360
TCTCCGCGCC	TGTCTGCACC	CTGTCGCCTG	AGCTGCCTGA	CAGTGACAAT	GACATCCCAG	420
TTACCAAGTG	CCTTGAATTG	ATAGTGGCTT	CTGTTTGTCA	GTCTCATATA	AGAACTACAG	480
CTCATCAGGA	GGAGATCGCA	GCAGGGTAAG	AGACACCAAC	ACCATGTTCT	GCACGAAGCT	540
CAAGGATCTC	AAGATCAGAG	GAGAGTGTCC	TTTCTCCTTA	CTGGCACCAG	GTCAAGTTCC	600
TAACGAGTCT	TCAGAGGAGG	CAGCAGGAAG	CTCAGAGAGC	TGCAAAGCAA	CCGTGCCCAT	660
CTGTCAAGAC	ATTCCCTGAGA	AGAACATACA	AGAAAGTCTT	CCTCAAAGAA	AAACCAAGTCG	720
GAGCCGAGTC	TATCTTCACA	CTTTGGCAGA	GAGTATTTGC	AAACTGATTT	TCCCAGAGTT	780
TGAACGGCTG	AATGTTGCAC	TTCAGAGAAC	ATTGGCAAAG	CACAAAATAA	AAGAAAGCAG	840
GAAATCTTTG	GAAAGAGAAG	ACTTTGAAAA	AACAATTGCA	GAGCAAGCAG	TTGCAGCAGG	900
AGTTCCAGTG	GAGGTTATCA	AAGAATCTCT	TGGTGAAGAG	GTTTTTAAAA	TATGTTACGA	960
GGAAGATGAA	AACATCCTTG	GGGTGGTTGG	AGGCACCCTT	AAAGATTTTT	TAAACAGCTT	1020

09/762767 2

CAGTACCCTT	CTGAAACAGA	GCAGCCATTG	CCAAGAAGCA	GGAAAAAGGG	GCAGGCTTGA	1080
GGACGCCTCC	ATTCTATGCC	TGGATAAGGA	GGATGATTTT	CTACATGTTT	ACTACTTCTT	1140
CCCTAAGAGA	ACCACCTCCC	TGATTCTTCC	CGGCATCATA	AAGGCAGCTG	CTCACGTATT	1200
ATATGAAACG	GAAGTGGAAG	TGTCGTTAAT	GCCTCCCTGC	TTCCATAATG	ATTGCAGCGA	1260
GTTTGTGAAT	CAGCCCTACT	TGTTGTACTC	CGTTCACATG	AAAAGCACCA	AGCCATCCCT	1320
GTCCCCCAGC	AAACCCCACT	CCTCGCTGGT	GATTCCCACA	TCGCTATTCT	GCAAGACATT	1380

delete all hard page  
breaks

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TCCATTCCAT	TTCATGTTTG	ACAAAGATAT	GACAATTCTG	CAATTTGGCA	ATGGCATCAG	1440
AAGGCTGATG	AACAGGAGAG	ACTTTCAAGG	AAAGCCTAAT	TTTGAAGAAT	ACTTTGAAAT	1500
TCTGACTCCA	AAAATCAACC	AGACGTTTAG	CGGGATCATG	ACTATGTTGA	ATATGCAGTT	1560
TGTTGTACGA	GTGAGGAGAT	GGGACAACCT	TGTGAAGAAA	TCTTCAAGGG	TTATGGACCT	1620
CAAAGGCCAA	ATGATCTACA	TTGTTGAATC	CAGTGCAATC	TTGTTTTTGG	GGTCACCCTG	1680
TGTGGACAGA	TTAGAAGATT	TTACAGGACG	AGGGCTCTAC	CTCTCAGACA	TCCCAATTCA	1740
CAATGCACTG	AGGGATGTGG	TCTTAATAGG	GGAAACAAGCC	CGAGCTCAAG	ATGGCCTGAA	1800
GAAGAGGCTG	GGGAAGCTGA	AGGCTACCCT	TGAGCAAGCC	CACCAAGCCC	TGGAGGAGGA	1860
GAAGAAAAAG	ACAGTAGACC	TTCTGTGCTC	CATATTTCCC	TGTGAGGTTG	CTCAGCAGCT	1920
GTGGCAAGGG	CAAGTTGTGC	AAGCCAAGAA	GTTCAGTAAT	GTCACCATGC	TCTTCTCAGA	1980
CATCGTTGGG	TTCAGTGCCA	TCTGCTCCCA	GTGCTCACCG	CTGCAGGTCA	TCACCATGCT	2040
CAATGCACTG	TACACTCGCT	TCGACCAGCA	GTGTGGAGAG	CTGGATGTCT	ACAAGGTGGA	2100
GACCATTGGC	GATGCCTATT	GTGTAGCTGG	GGGATTACAC	AAAGAGAGTG	ATACTCATGC	2160
TGTTTACGATA	GCGCTGATGG	CCCTGAAGAT	GATGGAGCTC	TCTGATGAAG	TTATGTCTCC	2220
CCATGGAGAA	CCTATCAAGA	TGCGAATTGG	ACTGCACTCT	GGATCAGTTT	TTGTGTGGCGT	2280
CGTTGGAGTT	AAAATGCCCC	GTTACTGTCT	TTTTGGAAAC	AATGTCACTC	TGGCTAACAA	2340
ATTTGAGTCC	TGCAGTGTAC	CACGAAAAAT	CAATGTCAAG	CCAACAACCT	ACAGATTACT	2400
CAAAGACTGT	CCTGGTTTTG	TGTTTACCCC	TCGATCAAGG	GAGGAACCTC	CACCAAACTT	2460
CCCTAGTGAA	ATCCCCGGAA	TCTGCCATTT	TCTGGATGCT	TACCAACAAG	GAACAAACTC	2520
AAAACCATGC	TTCCAAAAGA	AAGATGTGGA	AGATGGCAAT	GCCAATTTTT	TAGGCAAAGC	2580
ATCAGGAATA	GATTAGCAAC	CTATATACCT	ATTTATAAGT	CTTTGGGGTT	TGACTCATTG	2640
AAGATGTGTA	GAGCCTCTGA	AAGCACTTTA	GGGATTGTAG	ATGGCTAACA	AGCAGTATTA	2700
AAATTTTCAGG	AGCCAAGTCA	CAATCTTTCT	CCTGTTTAAAC	ATGACAAAAT	GTACTCACTT	2760
CAGTACTTCA	GCTCTTCAAG	AAAAAAAAAA	AAACCTTAAA	AAGCTACTTT	TGTGGGAGTA	2820
TTTCTATTAT	ATAACCAGCA	CTTACTACCT	GTACTCAAAA	TTCAGCACCT	TGTACATATA	2880
TCAGATAATT	GTAGTCAATT	GTACAAACTG	ATGGAGTCAC	CTGCAATCTC	ATATCCTGGT	2940
GGAATGCCAT	GGTTATTAAA	GTGTGTTTGT	GATAGTGTCT	TCAAAAAAAAA	AAAAAAAAAA	3000
AAAAAAAAAA	AAAAA					3015

(2) ~~DATA TO SEQ ID NO: 2~~ INFORMATION FOR SEQ ID NO: 2!

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGCal))

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Phe	Cys	Thr	Lys	Leu	Lys	Asp	Leu	Lys	Ile	Thr	Gly	Glu	Cys	Pro
				5					10					15	
Phe	Ser	Leu	Leu	Ala	Pro	Gly	Gln	Val	Pro	Asn	Glu	Ser	Ser	Glu	Glu
				20				25						30	
Ala	Ala	Gly	Ser	Ser	Glu	Ser	Cys	Lys	Ala	Thr	Val	Pro	Ile	Cys	Gln
				35				40						45	
Asp	Ile	Pro	Glu	Lys	Asn	Ile	Gln	Glu	Ser	Leu	Pro	Gln	Arg	Lys	Thr
				50				55						60	
Ser	Arg	Ser	Arg	Val	Tyr	Leu	His	Thr	Leu	Ala	Glu	Ser	Ile	Cys	Lys
				65				70						75	
Leu	Ile	Phe	Pro	Glu	Phe	Glu	Arg	Leu	Asn	Val	Ala	Leu	Gln	Arg	Thr
				85				90						95	
Leu	Ala	Lys	His	Lys	Ile	Lys	Glu	Ser	Arg	Lys	Ser	Leu	Glu	Arg	Glu
				100				105						110	
Asp	Phe	Glu	Lys	Thr	Ile	Ala	Glu	Gln	Ala	Val	Ala	Ala	Gly	Val	Pro
				115				120						125	
Val	Glu	Val	Ile	Lys	Glu	Ser	Leu	Gly	Glu	Glu	Val	Phe	Lys	Ile	Cys
				130				135						140	
Tyr	Glu	Glu	Asp	Glu	Asn	Ile	Leu	Gly	Val	Val	Gly	Gly	Thr	Leu	Lys
				145				150						155	
Asp	Phe	Leu	Asn	Ser	Phe	Ser	Thr	Leu	Leu	Lys	Gln	Ser	Ser	His	Cys

*follow these instructions throughout*

															165						170						175		
Gln	Glu	Ala	Gly	Lys	Arg	Gly	Arg	Leu	Glu	Asp	Ala	Ser	Ile	Leu	Cys														
			180							185				190															
Leu	Asp	Lys	Glu	Asp	Asp	Phe	Leu	His	Val	Tyr	Tyr	Phe	Phe	Pro	Lys														
			195				200				205																		
Arg	Thr	Thr	Ser	Leu	Ile	Leu	Pro	Gly	Ile	Ile	Lys	Ala	Ala	Ala	His														
			210				215				220																		
Val	Leu	Tyr	Glu	Thr	Glu	Val	Glu	Val	Ser	Leu	Met	Pro	Pro	Cys	Phe														
222	25				230				235				240																
His	Asn	Asp	Cys	Ser	Glu	Phe	Val	Asn	Gln	Pro	Tyr	Leu	Leu	Tyr	Ser														
			245				250				255																		
Val	His	Met	Lys	Ser	Thr	Lys	Pro	Ser	Leu	Ser	Pro	Ser	Lys	Pro	Gln														
			260				265				270																		
Ser	Ser	Leu	Val	Ile	Pro	Thr	Ser	Leu	Phe	Cys	Lys	Thr	Phe	Pro	Phe														
			275				280				285																		
His	Phe	Met	Phe	Asp	Lys	Asp	Met	Thr	Ile	Leu	Gln	Phe	Gly	Asn	Gly														
			290				300				305																		
Ile	Arg	Arg	Leu	Met	Asn	Arg	Arg	Asp	Phe	Gln	Gly	Lys	Pro	Asn	Phe														
310				315				320				325																	
Glu	Glu	Tyr	Phe	Glu	Ile	Leu	Thr	Pro	Lys	Ile	Asn	Gln	Thr	Phe	Ser														
			330				335				340																		
Gly	Ile	Met	Thr	Met	Leu	Asn	Met	Gln	Phe	Val	Val	Arg	Val	Arg	Arg														
			345				350				355																		
Trp	Asp	Asn	Ser	Val	Lys	Lys	Ser	Ser	Arg	Val	Met	Asp	Leu	Lys	Gly														
			360				365				370																		
Gln	Met	Ile	Tyr	Ile	Val	Glu	Ser	Ser	Ala	Ile	Leu	Phe	Leu	Gly	Ser														
			375				380				385																		
Pro	Cys	Val	Asp	Arg	Leu	Glu	Asp	Phe	Thr	Gly	Arg	Gly	Leu	Tyr	Leu														
390				395				400				405																	
Ser	Asp	Ile	Pro	Ile	His	Asn	Ala	Leu	Arg	Asp	Val	Val	Leu	Ile	Gly														
			410				415				420																		
Glu	Gln	Ala	Arg	Ala	Gln	Asp	Gly	Leu	Lys	Lys	Arg	Leu	Gly	Lys	Leu														
			425				430				435																		
Lys	Ala	Thr	Leu	Glu	Gln	Ala	His	Gln	Ala	Leu	Glu	Glu	Glu	Lys	Lys														
			440				445				450																		
Lys	Thr	Val	Asp	Leu	Leu	Cys	Ser	Ile	Phe	Pro	Cys	Glu	Val	Ala	Gln														
			455				460				465																		
Gln	Leu	Trp	Gln	Gly	Gln	Val	Val	Gln	Ala	Lys	Lys	Phe	Ser	Asn	Val														
470				475				480				485																	
Thr	Met	Leu	Phe	Ser	Asp	Ile	Val	Gly	Phe	Thr	Ala	Ile	Cys	Ser	Gln														
			490				495				500																		
Cys	Ser	Pro	Leu	Gln	Val	Ile	Thr	Met	Leu	Asn	Ala	Leu	Tyr	Thr	Arg														
			505				510				515																		
Phe	Asp	Gln	Gln	Cys	Gly	Glu	Leu	Asp																					

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Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu  
 630 635 640 645  
 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe  
 650 655 660  
 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys  
 665 670 675  
 Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly  
 680 685 690  
 Ile Asp  
 695

(2) DATA TO SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 basepairs  
 (B) TYPE: nucleotide  
 (C) STRANDEDNESS: doublestrand  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCCCCCG	CCGCTGCCGC	CTCTGCCTGG	GTCCCTTCGG	CCGTACCTCT	GCGTGGGGGC	60
TGCCTCCCCG	GCTCCCGGTG	CAGACACCAT	GTACGGATTT	GTGAATCACG	CCCTGGAGTT	120
GCTGGTGATC	CGCAATTACG	GCCCCGAGGT	GTGGGAAGAC	ATCAAAAAAG	AGGCACAGTT	180
AGATGAAGAA	GGACAGTTTC	TTGTCAGAAT	AATATATGAT	GACTCCAAAA	CTTATGATTT	240
GGTTGCTGCT	GCAAGCAAAG	TCCTCAATCT	CAATGCTGGA	GAAATCCTCC	AAATGTTTGG	300
GAAGATGTTT	TTCGTCTTTT	GCCAAGAATC	TGGTTATGAT	ACAATCTTGC	GTGTCCTGGG	360
CTCTAATGTC	AGAGAATTTT	TACAGAACCT	TGATGCTCTG	CACGACCACC	TTGCTACCAT	420
CTACCCAGGA	ATGCGTGCAC	CTTCCTTTAG	GTGCACTGAT	GCAGAAAAGG	GCAAAGGACT	480
CATTTTGCAC	TACTACTCAG	AGAGAGAAGG	ACTTCAGGAT	ATTGTCATTG	GAATCATCAA	540
AACAGTGGCA	CAACAAATCC	ATGGCACTGA	AATAGACATG	AAGGTTATTC	AGCAAAGAAA	600
TGAAGAATGT	GATCATACTC	AATTTTTAAT	TGAAGAAAAA	GAGTCAAAG	AAGAGGATTT	660
TTATGAAGAT	CTTGACAGAT	TTGAAGAAAA	TGGTACCCAG	GAATCACGCA	TCAGCCCATA	720
TACATTCTGC	AAAGCTTTTC	CTTTTCATAT	AATATTTGAC	CGGGACCTAG	TGGTCACTCA	780
GTGTGGCAAT	GCTATATACA	GAGTTCTCCC	CCAGCTCCAG	CCTGGGAATT	GCAGCCTTCT	840
GTCTGTCTTC	TCGCTGGTTC	GTCCTCATAT	TGATATTAGT	TTCCATGGGA	TCCTTTCTCA	900
CATCAATACT	GTTTTTGTAT	TGAGAAGCAA	GGAAGGATTG	TTGGATGTGG	AGAAATTAGA	960
ATGTGAGGAT	GAAGTACTG	GGACTGAGAT	CAGCTGCTTA	CGTCTCAAGG	GTCAAATGAT	1020
CTACTTACCT	GAAGCAGATA	GCATACTTTT	TCTATGTTCA	CCAAGTGTCA	TGAACCTGGA	1080
CGATTTGACA	AGGAGAGGGC	TGTATCTAAG	TGACATCCCT	CTGCATGATG	CCACGCGCGA	1140
TCTTGTTCTT	TTGGGAGAAC	AATTTAGAGA	GGAATACAAA	CTCACCCAAG	AACTGGAAAT	1200
CCTCACTGAC	AGGCTACAGC	TCACGTTAAG	AGCCCTGGAA	GATGAAAAGA	AAAAGACAGA	1260
CACATTGCTG	TATTCTGTCC	TTCCTCCGTC	TGTTGCCAAT	GAGCTGCGGC	ACAAGCGTCC	1320
AGTGCCTGCC	AAAAGATATG	ACAATGTGAC	CATCCTCTTT	AGTGGCATTG	TGGGCTTCAA	1380
TGCTTTCTGT	AGCAAGCATG	CATCTGGAGA	AGGAGCCATG	AAGATCGTCA	ACCTCCTCAA	1440
CGACCTCTAC	ACCAGATTTG	ACACACTGAC	TGATTCCCGG	AAAAACCCAT	TTGTTTATAA	1500
GGTGGAGACT	GTTGGTGACA	AGTATATGAC	AGTGAGTGGT	TTACCAGAGC	CATGCATTCA	1560
CCATGCACGA	TCCATCTGCC	ACCTGGCCTT	GGACATGATG	GAAATTGCTG	GCCAGGTTCA	1620
AGTAGATGGT	GAATCTGTTT	AGATAACAAT	AGGGATACAC	ACTGGAGAGG	TAGTTACAGG	1680
TGTCATAGGA	CAGCGGATGC	CTCGATACTG	TCTTTTTTGG	AATACTGTCA	ACCTCACAAAG	1740
CCGAACAGAA	ACCACAGGAG	AAAAGGGAAA	AATAAATGTG	TCTGAATATA	CATACAGATG	1800
TCTTATGTCT	CCAGAAAATT	CAGATCCACA	ATTCCACTTG	GAGCACAGAG	GCCCAGTGTC	1860
CATGAAGGGC	AAAAAAGAAC	CAATGCAAGT	TTGGTTTCTA	TCCAGAAAAA	ATACAGGAAC	1920
AGAGGAAACA	AAGCAGGATG	ATGACTGAAT	CTTGGATTAT	GGGGTGAAGA	GGAGTACAGA	1980
CTAGGTTCCA	GTTTTCTCCT	AACACGTGCC	AAGCCCAGGA	GCAGTTCCTC	CCTATGGATA	2040
CAGATTTTCT	TTTGTCTCTG	TCCATTACCC	CAAGACTTTT	TTCTAGATAT	ATCTCTCACT	2100
ATCCGTTATT	CAACCTTAGC	TCTGCTTTCT	ATTACTTTTT	AGGCTTTAGT	ATATTATCTA	2160
AAGTTTGGCT	TTTGATGTGG	ATGATGTGAG	CTTCATGTGT	CTTAAAATCT	ACTACAAGCA	2220
TTACCTAACA	TGGTGATCTG	CAAGTAGTAG	GCACCCAATA	AATATTTGTT	GAATTTAGTT	2280
AAATGAAACT	GAACAGTGTT	TGGCCATGTG	TATATTTATA	TCATGTTTAC	CAAATCTGTT	2340

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TAGTGTCCA CATATATGTA TATGTATATT TTAATGACTA TAATGTAATA AAGTTTATAT  
 CATGTTGGTG TATATCATTA TAGAAATCAT TTTCTAAAGG AGT

2400  
 2443

(2) DATA TO SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1 (hsGCbl))

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Tyr	Gly	Phe	Val	Asn	His	Ala	Leu	Glu	Leu	Leu	Val	Ile	Arg	Asn
				5					10					15	
Tyr	Gly	Pro	Glu	Val	Trp	Glu	Asp	Ile	Lys	Lys	Glu	Ala	Gln	Leu	Asp
			20				25						30		
Glu	Glu	Gly	Gln	Phe	Leu	Val	Arg	Ile	Ile	Tyr	Asp	Asp	Ser	Lys	Thr
		35					40					45			
Tyr	Asp	Leu	Val	Ala	Ala	Ala	Ser	Lys	Val	Leu	Asn	Leu	Asn	Ala	Gly
	50					55					60				
Glu	Ile	Leu	Gln	Met	Phe	Gly	Lys	Met	Phe	Phe	Val	Phe	Cys	Gln	Glu
	65				70					75					80
Ser	Gly	Tyr	Asp	Thr	Ile	Leu	Arg	Val	Leu	Gly	Ser	Asn	Val	Arg	Glu
			85						90					95	
Phe	Leu	Gln	Asn	Leu	Asp	Ala	Leu	His	Asp	His	Leu	Ala	Thr	Ile	Tyr
			100					105					110		
Pro	Gly	Met	Arg	Ala	Pro	Ser	Phe	Arg	Cys	Thr	Asp	Ala	Glu	Lys	Gly
		115					120					125			
Lys	Gly	Leu	Ile	Leu	His	Tyr	Tyr	Ser	Glu	Arg	Glu	Gly	Leu	Gln	Asp
	130					135					140				
Ile	Val	Ile	Gly	Ile	Ile	Lys	Thr	Val	Ala	Gln	Gln	Ile	His	Gly	Thr
	145				150					155				160	
Glu	Ile	Asp	Met	Lys	Val	Ile	Gln	Gln	Arg	Asn	Glu	Glu	Cys	Asp	His
			165						170					175	
Thr	Gln	Phe	Leu	Ile	Glu	Glu	Lys	Glu	Ser	Lys	Glu	Glu	Asp	Phe	Tyr
		180					185						190		
Glu	Asp	Leu	Asp	Arg	Phe	Glu	Glu	Asn	Gly	Thr	Gln	Glu	Ser	Arg	Ile
	195					200					205				
Ser	Pro	Tyr	Thr	Phe	Cys	Lys	Ala	Phe	Pro	Phe	His	Ile	Ile	Phe	Asp
	210					215					220				
Arg	Asp	Leu	Val	Val	Thr	Gln	Cys	Gly	Asn	Ala	Ile	Tyr	Arg	Val	Leu
	225				230				235					240	
Pro	Gln	Leu	Gln	Pro	Gly	Asn	Cys	Ser	Leu	Leu	Ser	Val	Phe	Ser	Leu
			245						250					255	
Val	Arg	Pro	His	Ile	Asp	Ile	Ser	Phe	His	Gly	Ile	Leu	Ser	His	Ile
		260						265					270		
Asn	Thr	Val	Phe	Val	Leu	Arg	Ser	Lys	Glu	Gly	Leu	Leu	Asp	Val	Glu
	275					280						285			
Lys	Leu	Glu	Cys	Glu	Asp	Glu	Leu	Thr	Gly	Thr	Glu	Ile	Ser	Cys	Leu
	290					295					300				
Arg	Leu	Lys	Gly	Gln	Met	Ile	Tyr	Leu	Pro	Glu	Ala	Asp	Ser	Ile	Leu
	305				310				315					320	
Phe	Leu	Cys	Ser	Pro	Ser	Val	Met	Asn	Leu	Asp	Asp	Leu	Thr	Arg	Arg
			325					330						335	
Gly	Leu	Tyr	Leu	Ser	Asp	Ile	Pro	Leu	His	Asp	Ala	Thr	Arg	Asp	Leu
		340					345						350		
Val	Leu	Leu	Gly	Glu	Gln	Phe	Arg	Glu	Glu	Tyr	Lys	Leu	Thr	Gln	Glu
	355						360					365			
Leu	Glu	Ile	Leu	Thr	Asp	Arg	Leu	Gln	Leu	Thr	Leu	Arg	Ala	Leu	Glu

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370	375	380
Asp Glu Lys Lys Lys Thr	Asp Thr Leu Leu Tyr	Ser Val Leu Pro Pro
385	390	395
Ser Val Ala Asn Glu Leu Arg His Lys Arg	Pro Val Pro Ala Lys Arg	400
	405	410
Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala		415
	420	425
Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn		430
	435	440
Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg		445
	450	455
Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met		460
465	470	475
Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile		480
	485	490
Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val		495
	500	505
Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val		510
	515	520
Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly		525
	530	535
Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly		540
545	550	555
Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu		560
	565	570
Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met		575
	580	585
Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn		590
	595	600
Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp Asp		605

(2) DATA TO SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGC1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro  
5 10

(2) DATA TO SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGC1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn  
5 10 15

Thr Gly Thr Glu Glu Thr

(2) DATA TO SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 basepairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single ~~strands~~

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC

28

(2) DATA TO SEQ ID NO: 8:

- ↑  
insert
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 basepairs
    - (B) TYPE: nucleotide
    - (C) STRANDEDNESS: single ~~strans~~
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTISENSE: no
  - (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

ATTATGGAAG CAGGGAGG

18

(2) DATA TO SEQ ID NO: 9:

- ↑
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 basepairs
    - (B) TYPE: nucleotide
    - (C) STRANDEDNESS: single ~~strans~~
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTISENSE: no
  - (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT

28

(2) DATA TO SEQ ID NO: 10:

- ↑
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 basepairs
    - (B) TYPE: nucleotide
    - (C) STRANDEDNESS: single ~~strans~~
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTISENSE: no
  - (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC

20

- 1) Please ensure all (A) LENGTH responses reflect actual number of bases or amino acids
- 2) all U.S. applications filed on or after July 1, 1998 and which cannot claim a prior application filed before July 1, 1998, need to be in new sequence rules format.